

## CRF Errors Corrected by the STIC Systems Branch

OIRE #5  
2113  
3/1/2002

Serial Number:

09/898,556A

CRF Processing Date:

Edited by:

Verified by:

(STIC staff)

Changed a file from non-ASCII to ASCII.

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

Edited a format error in the Current Application Data section, specifically:  
\_\_\_\_\_

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was  the prior application data; or  other \_\_\_\_\_.

Added the mandatory heading and subheadings for "Current Application Data".

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically:  
\_\_\_\_\_

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:  
\_\_\_\_\_

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:  
\_\_\_\_\_

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included:  
\_\_\_\_\_

Deleted extra, invalid, headings used by an applicant, specifically:  
\_\_\_\_\_

Deleted:  non-ASCII "garbage" at the beginning/end of files;  secretary initials/filename at end of file;  
 page numbers throughout text;  other invalid text, such as \_\_\_\_\_.

Inserted mandatory headings, specifically:  
\_\_\_\_\_

Corrected an obvious error in the response, specifically:  
\_\_\_\_\_

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically:  
\_\_\_\_\_

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_

Other:  
\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/898,556A

DATE: 03/07/2002

TIME: 19:05:08

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\03072002\I898556A.raw

3 <110> APPLICANT: C. Frank Bennett  
 4 Susan M. Freier  
 6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION  
 8 <130> FILE REFERENCE: RTS-0248  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/898,556A  
 C--> 10 <141> CURRENT FILING DATE: 2001-07-03  
 10 <160> NUMBER OF SEQ ID NOS: 89  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 20  
 15 <212> TYPE: DNA  
 16 <213> ORGANISM: Artificial Sequence  
 18 <220> FEATURE:  
 19 <223> OTHER INFORMATION: Antisense Oligonucleotide  
 21 <400> SEQUENCE: 1  
 22 tccgtcatcg ctcctcaggg 20  
 25 <210> SEQ ID NO: 2  
 26 <211> LENGTH: 20  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Artificial Sequence  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: Antisense Oligonucleotide  
 33 <400> SEQUENCE: 2  
 34 atgcattctg cccccaagga 20  
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 39 <211> LENGTH: 2772  
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 41 <213> ORGANISM: Homo sapiens  
 43 <220> FEATURE:  
 44 <221> NAME/KEY: CDS  
 45 <222> LOCATION: (3)...(2096)  
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 48 ca ggc gcg tta agc tgg ttg gga ccc ggg aag gcc tcc ctc tta agg 47  
 49 Gly Ala Leu Ser Trp Leu Gly Pro Gly Lys Ala Ser Leu Leu Arg  
 50 1 5 10 15  
 52 tct ttc cca cac ctc tgc tcc ttg tta cct gac ttt cgg ctt cag gat 95  
 53 Ser Phe Pro His Leu Cys Ser Leu Leu Pro Asp Phe Arg Leu Gln Asp  
 54 20 25 30  
 56 ccg cgg cgt gca ccc gcg ttc cat ctg tct tct gag act ttg ccc ttc 143  
 57 Pro Arg Arg Ala Pro Ala Phe His Leu Ser Ser Glu Thr Leu Pro Phe  
 58 35 40 45  
 60 tcc agg aag agc act cag gag acc agg aaa atg gct aca ggg ctc ctg 191  
 61 Ser Arg Lys Ser Thr Gln Glu Thr Arg Lys Met Ala Thr Gly Leu Leu  
 62 50 55 60

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| 64  | aga | gcc | aaa | aaa  | gag | gcg | ttc | gtg | gca | ttc | agg | gat | gtg | gct | gtg | tac | 239  |
| 65  | Arg | Ala | Lys | Lys  | Glu | Ala | Phe | Val | Ala | Phe | Arg | Asp | Val | Ala | Val | Tyr |      |
| 66  | 65  |     |     |      | 70  |     |     |     | 75  |     |     |     |     |     |     |     |      |
| 68  | ttc | acc | cag | gag  | gag | tgg | agg | ttg | ttg | agc | cct | gtc | cag | agg | acc | ctg | 287  |
| 69  | Phe | Thr | Gln | Glu  | Glu | Trp | Arg | Leu | Leu | Ser | Pro | Ala | Gln | Arg | Thr | Leu |      |
| 70  | 80  |     |     |      | 85  |     |     |     | 90  |     |     | 95  |     |     |     |     |      |
| 72  | cac | agg | gag | gtg  | atg | ctg | gag | act | tat | aac | cat | ctg | gtc | tca | ctg | gaa | 335  |
| 73  | His | Arg | Glu | Val  | Met | Leu | Glu | Thr | Tyr | Asn | His | Leu | Val | Ser | Leu | Glu |      |
| 74  |     |     |     |      | 100 |     |     |     | 105 |     |     | 110 |     |     |     |     |      |
| 76  | att | cca | tct | tct  | aaa | cca | aaa | ctc | att | gct | cag | ctg | gag | cga | ggg | gaa | 383  |
| 77  | Ile | Pro | Ser | Ser  | Lys | Pro | Lys | Leu | Ile | Ala | Gln | Leu | Glu | Arg | Gly | Glu |      |
| 78  |     |     |     |      | 115 |     |     |     | 120 |     |     | 125 |     |     |     |     |      |
| 80  | gcg | ccc | tgg | aga  | gag | gag | aga | aaa | tgt | cca | ctg | gac | ctc | tgt | cca | gaa | 431  |
| 81  | Ala | Pro | Trp | Arg  | Glu | Glu | Arg | Lys | Cys | Pro | Leu | Asp | Leu | Cys | Pro | Glu |      |
| 82  |     |     |     |      | 130 |     |     |     | 135 |     |     | 140 |     |     |     |     |      |
| 84  | tgc | aag | cca | gaa  | att | caa | ctt | agt | ccc | tcc | tgc | cct | ctg | att | ttc | tcc | 479  |
| 85  | Ser | Lys | Pro | Glu  | Ile | Gln | Leu | Ser | Pro | Ser | Cys | Pro | Leu | Ile | Phe | Ser |      |
| 86  |     |     |     |      | 145 |     |     |     | 150 |     |     | 155 |     |     |     |     |      |
| 88  | agt | cag | caa | gct  | ctc | agc | caa | cat | gtg | tgg | ctg | agt | cat | ctc | tct | cag | 527  |
| 89  | Ser | Gln | Gln | Ala  | Leu | Ser | Gln | His | Val | Trp | Leu | Ser | His | Leu | Ser | Gln |      |
| 90  | 160 |     |     |      | 165 |     |     |     | 170 |     |     | 175 |     |     |     |     |      |
| 92  | ctg | ttt | tca | agt  | tta | tgg | gca | gga | aat | cct | ctc | cac | ctg | gga | aaa | cac | 575  |
| 93  | Leu | Phe | Ser | Ser  | Leu | Trp | Ala | Gly | Asn | Pro | Leu | His | Leu | Gly | Lys | His |      |
| 94  |     |     |     |      | 180 |     |     |     | 185 |     |     | 190 |     |     |     |     |      |
| 96  | tat | cca | gaa | .gat | cag | aaa | caa | cag | cag | gat | cca | ttc | tgc | ttt | agt | ggc | 623  |
| 97  | Tyr | Pro | Glu | Asp  | Gln | Lys | Gln | Gln | Asp | Pro | Phe | Cys | Phe | Ser | Gly |     |      |
| 98  |     |     |     |      | 195 |     |     |     | 200 |     |     | 205 |     |     |     |     |      |
| 100 | aaa | gca | gaa | tgg  | att | caa | gag | gga | gaa | gac | tcc | aga | ctc | ctg | ttt | ggg | 671  |
| 101 | Lys | Ala | Glu | Trp  | Ile | Gln | Glu | Gly | Glu | Asp | Ser | Arg | Leu | Leu | Phe | Gly |      |
| 102 |     |     |     |      | 210 |     |     |     | 215 |     |     | 220 |     |     |     |     |      |
| 104 | aga | gta | agc | aaa  | aat | ggc | act | tca | aag | gca | ctt | tcc | agc | ccā | cct | gaa | 719  |
| 105 | Arg | Val | Ser | Lys  | Asn | Gly | Thr | Ser | Lys | Ala | Leu | Ser | Ser | Pro | Pro | Glu |      |
| 106 |     |     |     |      | 225 |     |     |     | 230 |     |     | 235 |     |     |     |     |      |
| 108 | gaa | caa | cag | cca  | gca | cag | tcc | aag | gaa | gac | aac | aca | gtg | gtg | gat | ata | 767  |
| 109 | Glu | Gln | Gln | Pro  | Ala | Gln | Ser | Lys | Glu | Asp | Asn | Thr | Val | Val | Asp | Ile |      |
| 110 | 240 |     |     |      | 245 |     |     |     | 250 |     |     | 255 |     |     |     |     |      |
| 112 | ggg | tcc | agc | cct  | gaa | cgg | agg | gca | gat | cta | gag | gaa | aca | gac | aaa | gta | 815  |
| 113 | Gly | Ser | Ser | Pro  | Glu | Arg | Arg | Ala | Asp | Leu | Glu | Glu | Thr | Asp | Lys | Val |      |
| 114 |     |     |     |      | 260 |     |     |     | 265 |     |     | 270 |     |     |     |     |      |
| 116 | ttg | cat | ggt | tta  | gaa | gtc | tca | gga | ttt | gga | gaa | atc | aaa | tat | gaa | gag | 863  |
| 117 | Leu | His | Gly | Leu  | Glu | Val | Ser | Gly | Phe | Gly | Glu | Ile | Lys | Tyr | Glu | Glu |      |
| 118 |     |     |     |      | 275 |     |     |     | 280 |     |     | 285 |     |     |     |     |      |
| 120 | ttt | ggg | cca | ggc  | ttt | atc | aag | gag | tca | aac | ctc | ctt | agc | ctc | cag | aag | 911  |
| 121 | Phe | Gly | Pro | Gly  | Phe | Ile | Lys | Glu | Ser | Asn | Leu | Leu | Ser | Leu | Gln | Lys |      |
| 122 |     |     |     |      | 290 |     |     |     | 295 |     |     | 300 |     |     |     |     |      |
| 124 | aca | caa | act | ggg  | gag | aca | cct | tac | atg | tac | act | gag | tgg | gga | gac | agc | 959  |
| 125 | Thr | Gln | Thr | Gly  | Glu | Thr | Pro | Tyr | Met | Tyr | Thr | Glu | Trp | Gly | Asp | Ser |      |
| 126 |     |     |     |      | 305 |     |     |     | 310 |     |     | 315 |     |     |     |     |      |
| 128 | ttt | ggc | agt | atg  | tca | gtc | ctc | atc | aaa | aac | cca | agg | aca | cac | tct | ggg | 1007 |

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| 129 Phe | Gly | Ser | Met | Ser | Val | Leu | Lys | Asn | Pro | Arg | Thr | His | Ser | Gly |     |      |
| 130 320 |     |     |     | 325 |     |     | 330 |     |     |     |     |     |     | 335 |     |      |
| 132 gga | aag | cct | tat | gtg | tgc | agg | gaa | tgt | ggg | cga | ggc | ttt | acg | tgg | aag | 1055 |
| 133 Gly | Lys | Pro | Tyr | Val | Cys | Arg | Glu | Cys | Gly | Arg | Gly | Phe | Thr | Trp | Lys |      |
| 134     |     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |      |
| 136 tca | aac | ctg | atc | aca | cat | cag | agg | aca | cac | tca | ggg | gag | aaa | cct | tat | 1103 |
| 137 Ser | Asn | Leu | Ile | Thr | His | Gln | Arg | Thr | His | Ser | Gly | Glu | Lys | Pro | Tyr |      |
| 138     |     |     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |      |
| 140 gtg | tgc | aag | gat | tgt | gga | cga | ggc | ttt | act | tgg | aag | tcg | aac | ctc | ttt | 1151 |
| 141 Val | Cys | Lys | Asp | Cys | Gly | Arg | Gly | Phe | Thr | Trp | Lys | Ser | Asn | Leu | Phe |      |
| 142     |     |     |     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |      |
| 144 aca | cat | cag | cgg | aca | cac | tca | ggg | ctc | aag | cct | tat | gtg | tgc | aag | gaa | 1199 |
| 145 Thr | His | Gln | Arg | Thr | His | Ser | Gly | Leu | Lys | Pro | Tyr | Val | Cys | Lys | Glu |      |
| 146     |     |     |     | 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |      |
| 148 tgt | ggg | cag | agc | ttt | agc | ctg | aag | tca | aac | ctc | att | acc | cac | cag | agg | 1247 |
| 149 Cys | Gly | Gln | Ser | Phe | Ser | Leu | Lys | Ser | Asn | Ile | Thr | His | Gln | Arg |     |      |
| 150 400 |     |     |     |     | 405 |     |     |     | 410 |     |     |     |     | 415 |     |      |
| 152 gcg | cac | act | ggg | gag | aag | cct | tat | gtt | tgc | agg | gaa | tgt | ggg | cgt | ggc | 1295 |
| 153 Ala | His | Thr | Gly | Glu | Lys | Pro | Tyr | Val | Cys | Arg | Glu | Cys | Gly | Arg | Gly |      |
| 154     |     |     |     | 420 |     |     |     | 425 |     |     |     |     |     | 430 |     |      |
| 156 ttt | cgc | cag | cat | tca | cac | ctg | gtc | aga | cac | aag | agg | aca | cat | tca | gga | 1343 |
| 157 Phe | Arg | Gln | His | Ser | His | Leu | Val | Arg | His | Lys | Arg | Thr | His | Ser | Gly |      |
| 158     |     |     |     | 435 |     |     |     | 440 |     |     |     |     |     | 445 |     |      |
| 160 gag | aag | cct | tac | att | tgc | agg | gag | tgt | gag | caa | ggc | ttt | agc | cag | aag | 1391 |
| 161 Glu | Lys | Pro | Tyr | Ile | Cys | Arg | Glu | Cys | Glu | Gln | Gly | Phe | Ser | Gln | Lys |      |
| 162     |     |     |     | 450 |     |     |     | 455 |     |     |     |     |     | 460 |     |      |
| 164 tca | cac | ctc | atc | aga | cac | tta | agg | aca | cac | aca | gga | gag | aag | cct | tat | 1439 |
| 165 Ser | His | Leu | Ile | Arg | His | Leu | Arg | Thr | His | Thr | Gly | Glu | Lys | Pro | Tyr |      |
| 166     |     |     |     | 465 |     |     |     | 470 |     |     |     |     |     | 475 |     |      |
| 168 gta | tgc | aca | gaa | tgt | ggg | cgt | cac | ttt | agc | tgg | aaa | tca | aac | ctc | aaa | 1487 |
| 169 Val | Cys | Thr | Glu | Cys | Gly | Arg | His | Phe | Ser | Trp | Lys | Ser | Asn | Leu | Lys |      |
| 170 480 |     |     |     |     | 485 |     |     |     | 490 |     |     |     |     | 495 |     |      |
| 172 aca | cac | cag | aca | cac | tca | ggg | gtt | aaa | cct | tat | gtc | tgc | ctg | gag |     | 1535 |
| 173 Thr | His | Gln | Arg | Thr | His | Ser | Gly | Val | Lys | Pro | Tyr | Val | Cys | Leu | Glu |      |
| 174     |     |     |     | 500 |     |     |     | 505 |     |     |     |     |     | 510 |     |      |
| 176 tgc | ggg | cag | tgc | ttt | agc | ctg | aag | tca | aac | ctt | aaa | cac | cag | agg |     | 1583 |
| 177 Cys | Gly | Gln | Cys | Phe | Ser | Leu | Lys | Ser | Asn | Leu | Asn | Lys | His | Gln | Arg |      |
| 178     |     |     |     | 515 |     |     |     | 520 |     |     |     |     |     | 525 |     |      |
| 180 tca | cac | acg | ggg | gag | aag | cca | ttt | gta | tgt | acg | gag | tgt | ggg | cga | ggc | 1631 |
| 181 Ser | His | Thr | Gly | Glu | Lys | Pro | Phe | Val | Cys | Thr | Glu | Cys | Gly | Arg | Gly |      |
| 182     |     |     |     | 530 |     |     |     | 535 |     |     |     |     |     | 540 |     |      |
| 184 ttt | acc | cgg | aaa | tca | acc | ctg | atc | acg | cac | cag | agg | aca | cac | tca | ggg | 1679 |
| 185 Phe | Thr | Arg | Lys | Ser | Thr | Leu | Ile | Thr | His | Gln | Arg | Thr | His | Ser | Gly |      |
| 186     |     |     |     | 545 |     |     |     | 550 |     |     |     |     |     | 555 |     |      |
| 188 gag | aag | cca | ttt | gta | tgt | gct | gag | tgt | gga | cga | ggc | ttt | aat | gat | aag | 1727 |
| 189 Glu | Lys | Pro | Phe | Val | Cys | Ala | Glu | Cys | Gly | Arg | Gly | Phe | Asn | Asp | Lys |      |
| 190 560 |     |     |     |     | 565 |     |     |     | 570 |     |     |     |     | 575 |     |      |
| 192 tcc | acc | ctc | att | tca | cac | cag | agg | aca | cat | tca | ggg | gaa | aag | cct | ttt | 1775 |
| 193 Ser | Thr | Leu | Ile | Ser | His | Gln | Arg | Thr | His | Ser | Gly | Glu | Lys | Pro | Phe |      |

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| 196 atg tgc agg gag tgt ggc aga agg ttt cgg cag aag cct aac ctg ttt      |     |     |     | 1823 |
| 197 Met Cys Arg Glu Cys Gly Arg Arg Phe Arg Gln Lys Pro Asn Leu Phe      |     |     |     |      |
| 198 595  | 600 | 605 |     |      |
| 200 agg cac aag agg gca cac tca ggt gcc ttt gtg tgc agg gag tgt ggg      |     |     |     | 1871 |
| 201 Arg His Lys Arg Ala His Ser Gly Ala Phe Val Cys Arg Glu Cys Gly      |     |     |     |      |
| 202 610  | 615 | 620 |     |      |
| 204 caa ggc ttt tgt gct aag tta act ctc att aaa cac cag aga gca cac      |     |     |     | 1919 |
| 205 Gln Gly Phe Cys Ala Lys Leu Thr Leu Ile Lys His Gln Arg Ala His      |     |     |     |      |
| 206 625  | 630 | 635 |     |      |
| 208 gca ggg ggg aag cct cat gtg tgc agg gag tgt ggg caa ggc ttt agc      |     |     |     | 1967 |
| 209 Ala Gly Gly Lys Pro His Val Cys Arg Glu Cys Gly Gln Gly Phe Ser      |     |     |     |      |
| 210 640  | 645 | 650 | 655 |      |
| 212 cgg cag tca cac ctc att aga cac cag agg aca cat tca gga gag aag      |     |     |     | 2015 |
| 213 Arg Gln Ser His Leu Ile Arg His Gln Arg Thr His Ser Gly Glu Lys      |     |     |     |      |
| 214 660  | 665 | 670 |     |      |
| 216 cct tat att tgc aga aag tgt gga cgg ggc ttt agt cgg aag tcc aac      |     |     |     | 2063 |
| 217 Pro Tyr Ile Cys Arg Lys Cys Gly Arg Gly Phe Ser Arg Lys Ser Asn      |     |     |     |      |
| 218 675  | 680 | 685 |     |      |
| 220 ctt atc aga cat cag agg aca cac tca gga tag aaactttatg tgtataggaa    |     |     |     | 2116 |
| 221 Leu Ile Arg His Gln Arg Thr His Ser Gly                              |     |     |     |      |
| 222 690  | 695 |     |     |      |
| 224 atgtggtaca gccttagcc aggagtata cttcatcaga caccagagga cacacacagt      |     |     |     | 2176 |
| 226 gctgtggctt ttccagccat tgctagatac caaagtggag acattctgtg tgtgattatg    |     |     |     | 2236 |
| 228 catgagactg tactggtaag acttgtatct ccattcacct gaaggagaat tgctggctca    |     |     |     | 2296 |
| 230 ttttcaggag ccctgccctt cctcaactgtg gatgggtgggt tgtggaaacc cggtcaggt   |     |     |     | 2356 |
| 232 atgatagtgg caggaggcag tcaaatgccc aggcagatag ggggtgggtac ctggtgaaac   |     |     |     | 2416 |
| 234 ccaaccttaa agctgaagac agtcccggct aaatcctcat actgaattga gaacctgtct    |     |     |     | 2476 |
| 236 tccccatttgg tgtgcttcc tccgattgtat ccccaaccctt cacctatttt acgtataacct |     |     |     | 2536 |
| 238 gcccatttc aattggttt tacactgtg tgcccacctt ttgagtggtg cctttgcata       |     |     |     | 2596 |
| 240 cttacaaatc agtcaacgtg tattcccta ttctgagccc ataaaagacc cagactcagc     |     |     |     | 2656 |
| 242 tgcagtgagg agagaaaatca ccctgctgtg gaggtgggg accactccct gcataccctc    |     |     |     | 2716 |
| 244 tccactgaga gctgttctt tgctcaataa aattctttc taccatccct caccct          |     |     |     | 2772 |
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| 248 <211> LENGTH: 21   |     |     |     |      |
| 249 <212> TYPE: DNA  |     |     |     |      |
| 250 <213> ORGANISM: Artificial Sequence                                  |     |     |     |      |
| 252 <220> FEATURE:   |     |     |     |      |
| 253 <223> OTHER INFORMATION: PCR Primer                                  |     |     |     |      |
| 255 <400> SEQUENCE: 4  |     |     |     |      |
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| 259 <210> SEQ ID NO: 5   |     |     |     |      |
| 260 <211> LENGTH: 19   |     |     |     |      |
| 261 <212> TYPE: DNA  |     |     |     |      |
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| 264 <220> FEATURE:   |     |     |     |      |
| 265 <223> OTHER INFORMATION: PCR Primer                                  |     |     |     |      |
| 267 <400> SEQUENCE: 5  |     |     |     |      |
| 268 acctgaccgg gtttccaca   |     |     |     | 19   |

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| 271 <210> SEQ ID NO: 6  |     |
| 272 <211> LENGTH: 25  |     |
| 273 <212> TYPE: DNA   |     |
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| 276 <220> FEATURE:  |     |
| 277 <223> OTHER INFORMATION: PCR Probe                                    |     |
| 279 <400> SEQUENCE: 6   |     |
| 280 ctgcccttcc tcactgtgga tggtg   | 25  |
| 283 <210> SEQ ID NO: 7  |     |
| 284 <211> LENGTH: 19  |     |
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| 286 <213> ORGANISM: Artificial Sequence                                   |     |
| 288 <220> FEATURE:  |     |
| 289 <223> OTHER INFORMATION: PCR Primer                                   |     |
| 291 <400> SEQUENCE: 7   |     |
| 292 gaaggtaag gtcggagt  | 19  |
| 295 <210> SEQ ID NO: 8  |     |
| 296 <211> LENGTH: 20  |     |
| 297 <212> TYPE: DNA   |     |
| 298 <213> ORGANISM: Artificial Sequence                                   |     |
| 300 <220> FEATURE:  |     |
| 301 <223> OTHER INFORMATION: PCR Primer                                   |     |
| 303 <400> SEQUENCE: 8   |     |
| 304 gaagatggtg atgggattc  | 20  |
| 307 <210> SEQ ID NO: 9  |     |
| 308 <211> LENGTH: 20  |     |
| 309 <212> TYPE: DNA   |     |
| 310 <213> ORGANISM: Artificial Sequence                                   |     |
| 312 <220> FEATURE:  |     |
| 313 <223> OTHER INFORMATION: PCR Probe                                    |     |
| 315 <400> SEQUENCE: 9   |     |
| 316 caagcttccc gttctcagcc   | 20  |
| 319 <210> SEQ ID NO: 10   |     |
| 320 <211> LENGTH: 11173   |     |
| 321 <212> TYPE: DNA   |     |
| 322 <213> ORGANISM: Homo sapiens  |     |
| 324 <220> FEATURE:  |     |
| 326 <400> SEQUENCE: 10  |     |
| 327 aagttcttg gctctctaag ttttattttc tattcactgt gagaagtact tggctattat      | 60  |
| 329 ttcaatattt ttccctgtccc ttttactctt tcctctcatt ctaggactcc caatttacct    | 120 |
| 331 gtatatttggaa ctgctggaaa tgtgtttctg aagattcata ttgtctcata agcttctgtt   | 180 |
| 333 catttttctt cagtttttt tcttttttt gaggggtggg tggatatatg taatttctat       | 240 |
| 335 tcttttattt tcaaattcac taatctttct tcttttctg tttgcatttta aacctgtcta     | 300 |
| 337 gtgaattttt aaatttcagt ttttttttc ttccccctc ccctccctc ccctccctc         | 360 |
| 339 ccctccccctc ccctccccctc ccctccccctc ccctccccctc ccctccctc ctcttgcattt | 420 |
| 341 tgtgggtttt aggagtgcgc tcaggcaaga aagccacaaa caaaattatt acccctttct     | 480 |
| 343 gttgcaattt tttgagcata aactcttccc catcttctgg ctggttatgt atattttcca     | 540 |
| 345 gtgcctttga gtagtttattt gttatattt atccagtcattt attatttctt gctgcagggt   | 600 |
| 347 tcttgtgacc atttcagtcattt gctggcattt tcgttagtgg gcttcctcat acttattttt  | 660 |

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/898,556A

DATE: 03/07/2002

TIME: 19:05:09

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\03072002\I898556A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date